

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit  
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MPsrch_pp  protein - protein database search, using Smith-Waterman algorithm
Run on:      Sat May 13 10:04:54 2000;  MasPar time 3.95 Seconds
Tabular output not generated.  257.923 Million cell updates/sec

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Title: >US-09-331-631-3
Description: (74-116) From US0931631.pep (3 of 5)
Perfect Score: 344
Sequence: 1 NDDPDPTDCQQCCQRCRCRQDESGEPQQOYQCRCKETCEEHEEY 43

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Scoring table: PAM 150  
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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Database: a-geneseq35
          1:geneseqp
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Statistics: Mean 22.293; Variance 94.911; scale 0.2335

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description	Pred.	No.
1	344	100.0	666	1	W62829	Macadamia integrifolia	5.65e-24	
2	342	99.4	666	1	W62828	Macadamia integrifolia	8.81e-24	
3	335	97.4	625	1	W62830	Macadamia integrifolia	4.18e-23	
4	159	46.2	525	1	W62831	Theobroma cacao antim	1.70e-06	
5	159	46.2	566	1	R20181	Sequence encoded by 67	1.70e-06	
6	127	35.9	590	1	W62832	Gossypium hirsutum ant	1.24e-03	
7	111	32.3	28	1	W62841	Stenocarpus sinuatus a	3.08e-02	
8	111	32.3	593	1	W62835	zea may antimicrobial	3.08e-02	
9	105	30.5	33	1	W62836	zea may antimicrobial	1.01e-01	
10	96	27.9	35	1	R21079	antimicrobial maize pe	5.81e-01	
11	85	24.7	637	1	W62837	Hordeum vulgare antim	4.72e-00	
12	83	24.1	106	1	R91706	ACANP21.	6.86e+00	
13	83	24.1	107	1	R91705	ACANP23.	6.86e+00	
14	82	23.8	626	1	W21550	Peanut allergen Ara hi	8.27e+00	
15	79	23.0	441	1	R85214	Peroxisome proliferat	1.44e+01	
16	79	23.0	441	1	R81875	Steroid hormone recept	1.44e+01	
17	77	22.4	614	1	W62834	Arachis hypogaea antim	2.08e+01	
18	77	22.4	614	1	W22149	Peanut allergen Ara hi	2.08e+01	
19	77	22.4	910	1	R91737	HER4-Ig fusion protein	2.08e+01	
20	77	22.4	1058	1	R54843	HER4 with alternate 3'	2.08e+01	
21	77	22.4	1058	1	R91734	Receptor tyrosine kina	2.08e+01	
22	77	22.4	1308	1	R54841	HER4.	2.08e+01	
23	77	22.4	1308	1	R91733	Receptor tyrosine kina	2.08e+01	

5	1003	1	R55576	Ampev spheroideidin.	1.05e+02
6	19.8	1			
7	68	15.8			
8	68	15.8			
9	68	15.8			
10	44	461	1R97982	Human steroid receptor	1.05e+02
11	43	461	1R56234	Human foetal lung ster	1.05e+02
12	42	898	1M1853	Mycobacterium tubercu	8.33e+01
13	41	20.1			
14	39	402	1W57410	Human Ery-1 receptor	8.33e+01
15	39	20.1			
16	39	20.1			
17	38	20.1			
18	69	204	1M59609	DNA-binding/dimerizat	8.33e+01
19	37	1786	1W50893	Human laminin B1 chain	8.33e+01
20	70	20.3			
21	71	20.6	1R38209	APL EGF recep	6.18e+01
22	35	529	1R38209	LDL2D23	7.39e+01
23	34	509	1W33737	Epidermal growth facto	6.18e+01
24	34	509	1R38121	LDPD34	6.18e+01
25	33	71			
26	72	20.9	1R14053	Human pteroxisome proli	5.16e+01
27	32	20.9	1R14053	Human pteroxisome proli	5.16e+01
28	33	72	1F01362	Soybean glycinin A5B4	5.16e+01
29	35	509	1W33737	Epidermal growth facto	6.18e+01
30	34	509	1R38121	LDPD34	6.18e+01
31	34	509	1R38209	LDL2D23	7.39e+01
32	71	20.6	1R38209	APL EGF recep	6.18e+01
33	71	20.6	1R38209	LDL2D23	7.39e+01
34	71	20.6	1R38209	LDL2D23	7.39e+01
35	70	20.3			
36	37	1786	1W50893	Human laminin B1 chain	8.33e+01
37	69	20.1			
38	69	20.1			
39	69	20.1			
40	41	898	1M1853	Mycobacterium tubercu	8.33e+01
41	42	19.8			
42	43	461	1R56234	Human foetal lung ster	1.05e+02
43	44	461	1R97982	Human steroid receptor	1.05e+02
44	68	15.8			
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302	68	15.8			
303	68				

## ALIGNMENTS

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RESULT 1
ID W62829 standard; Protein: 666 AA.
AC W62829.
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key Location/Qualifiers
FT Peptide 1..28
FT Protein /note="signal peptide"
FT Protein /note="mature protein"
PN W09827805.A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Gaultier KC, Green JL, Manners JM, Marcus JP;
PI WPI: 98-3/72/9/32.
DR N-PSD: V42311.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PT Claim 1: Page 39-41: 96pp: English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
CC Sequence 666 AA;
SQ
Query Match 100.0% Score 344; DB 1; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.65e-24;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db 74 NQDDPQTDCCQCCQRRCRQESGSPRQQVCCQRCKEICEEEHEEY 116
|||
Oy 74 NQDDPQTDCCQCCQRRCRQESGSPRQQVCCQRCKEICEEEHEEY 116

RESULT 2
ID W62828 standard; Protein: 666 AA.
AC W62828.
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key Location/Qualifiers
FT Peptide 1..28
FT Protein /note="signal peptide"
FT Protein /note="mature protein"
PN W09827805.A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Gaultier KC, Green JL, Manners JM, Marcus JP;
PI WPI: 98-3/72/9/32.
DR N-PSD: V42311.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PT Claim 1: Page 39-41: 96pp: English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
CC Sequence 666 AA;
SQ
Query Match 100.0% Score 344; DB 1; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.65e-24;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Db 74 NQDDPQTDCCQCCQRRCRQESGSPRQQVCCQRCKEICEEEHEEY 116
|||
Oy 74 NQDDPQTDCCQCCQRRCRQESGSPRQQVCCQRCKEICEEEHEEY 116

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